

FIGURE 1

CCAGGTCCAAC TGCACCTCGGTTCTATCGATTGAATTC CCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCAGGACACAGCAGCGGCCACCATGGCCACGCTTGGGC
TCCAGCAGCATCAGCAGCCCCAGGACCGGGGAGGCACAGGTGGCCCCACCCACCCGGAGG
AGCAGCTCCTGCCCTGTCCGGGGGATGACTGATTCTCTCCGCCAGGCCACCCAGAGGAGA
AGGCCACCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT
TCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCCTACCGGCCCGGCCGTTAGGGTGTGTGCT
GTCCCGGGCTCACGGGGACCTGTCTCCGAGTCGTTGTCGACGCTGTGTACCAGCCCTTCC
TCACCACTGCGACGGGCACCGGGCTGCAGCACCTACCGAACCATTTATAGGACCGCCTAC
CGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGTACGCGTGCTGCCCGGCTGGAAGAG
GACCAGCGGGCTTCTTGGGCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAG
GGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG
TCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCAGCGCTGCATCAACACCGC
CGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG
TGCCCAAGGAGGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAG
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCT
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC
TCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCCTTC
CTGGAGGAGCAGCTGGGGTCTGTCTCCTGCAAGAAAGACTCGTGAGACTGCCAGCGCCCAGG
CTGGACTGAGCCCTCACGCCGCCCTGCAGCCCCATGCCCTGCCCAACATGCTGGGGGTC
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCCTTTTCTCCTC
CCCTTCCCTCGGGAGGGTCCCCAGACCCTGGCATGGGATGGGCTGGGATTTTTTTTGTGAAT
CCACCCCTGGCTACCCCCACCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCCA
GCTGAGGGAAGGTACGAGTTCCTTGTGAGCCTGGGACCCATGGCAGGCCAGGCAGCC
CGGAGGCTGGGTGGGGCCTCAGTGGGGCTGCTGCCTGACCCCGACACAATAAAATGAAA
CGTGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGCGGCCGCGACTCT
AGAGTCGACCTGCAGAAGCTTGGCCGCATGGCCCAACTGTGTTATTGCAGCTTATAATGGT
TACAAAT

FIGURE 2

MTDSPPPGHPPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSTRAHGDPV
SESFVQRVYQPFLLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC
GAAICQPPCRNGGSCVQPGRCRCPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCW
EGHSLSADGTLCPVKGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLAS
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 93-97, 270-274

N-myristoylation sites.

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,
191-197, 265-271

Amidation site.

amino acids 26-30

Aspartic acid and asparagine hydroxylation site.

amino acids 152-164

Cell attachment sequence.

amino acids 130-133

EGF-like domain cysteine pattern signature.

amino acids 123-135

FIGURE 3

CGCTCGCCCCGTCGCCCTCGCCTCCCCGCAGAGTCCCCTCGCGGCAGCAGATGTGTGTGGG
GTCAGCCACGCGCGGGGACTATGTGTAATTCCTCGGCGCTCACGCACACTACTGGCCCCGTATC
CGGTTCTTGGTGCCCCGCGCATCAACACATAGCCCTCTGTGTATGGTGTGGCAGGGGCCATCGC
CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGTT
ACTCCCTCATGAAGTCTCTTACGGGTCCCATGAGTGACTTCAAAAATGTGGGCCTGGTGT
GTGAACAGCAAGAGACAGGACGAGCAAGAGCCCTCTGTGTATGGTGTGGCAGGGGCCATCGC
TGCCGCTCTTTACACACATGATAGCTTATAGTGATTTAGGATACTCATATATCAATAAATCTTC
ACCATTGTGACGAGTCCGTGGGGAGCAAGACGAGAAGGGCCCTCTGTACTCTCGCCGCTTC
CCTTTATGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAACACAAATACAGTTT
CCTGGTGGGATGTGCCTCAATCTCAGATGTCATAGCTCAGGTGTGTTTTGTAGCCATTTTGC
TTCACAGTCACCTGGAATGCCGGAGCCCCCTGCTCATCCCGATCCTCTCCTTGATACATGGGC
GCACCTGTGTGCGCTGCACACCCCTGTGCCTGGGCTACTACAAGAACATTACGACATCATCCC
TGACAGAAGTGGCCCCGAGCTGGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT
GGCCTTTGGCTCTAATTTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCGGGAGCTTGGTGCGAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTGTGGGTCACATGCCATCCGCTGGTTGACGGAAATCCGTGCTGTGTATCTCTGTTTCG
ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACAGTCACGGCAGCCCCACATC
AAGAAGTTACCTTTCGTCTGCATGGCTCTGTCACTCAGCTCTGTTCGTGATGTTTTGGAC
ACCCAACGTGTCTGAGAAAATCTTGATAGACATCATCGGAGTGGACTTTGGCTTTTGAGAAC
TCTGTGTGTCTCTTTGCGGATCTCTCCTCTCTCCAGTTCCAGTCACAGTGAAGGGCGCAT
CTCACCGGTGGCTGATGACACTGAAGAAAACCTTCGCTCTTGCCCCAGCTCTGTGCTCGG
GGCATCGCTCTCATCGCCAGCCTCGTGGTCTTACCCTACTCGGGGGTGACGGTGGCAGCC
TGGGCTGGGCTCCCTCTCGCGGGCTTTGTGGGAGAATCCACCATGGTGCCTCATCGCTCGG
TGCTATGTCTACCGAAGCGAAAAAGAAGATGGAGAATGAGTCGGCCACGGAGGGGGAAGA
CTCTGCCATGACAGACATGCCTCCGACAGAGGAGGTGACAGACATCGTGGAAATGAGAGAGG
AGAATGAATAAAGGACGCGGACGCCATGGGCACTGCAGGACGGTCAGTCAGGATGACACTTC
GGCATCATCTCTCCCTCTCCATCGTATTTGTTCCTCTTTTTTTGTTTTGTTTTGGTAAT
GAAAGAGGCCCTTGATTTAAAGGTTTCGTGTCAATTTCTCTAGCATACTGGGTATGCTCACACT
GACGGGGGACCTAGTGAATGGTCTTTACTGTGCTATGTAAAAACAAACGAAACAACTGAC
TTCATACCCCTGCCTCACGAAAAACCAAAGACACAGCTGCCTCACGGTTGACGTTTGTGTCT
TCCCTCCCTGGACAATCTCTCTTGGAACCAAAGGACTGCAGCTGTGCCATCGCCGCTCGGT
CACCTTCACAGCGAGCCACAGACTCTCCTGTCCCCCTCATCGCTCTTAAGAATCAACAGG
TTAAAACTCGGCTTCTTTGATTGTCTTCCAGTCACATGGCCGTACAAGAGATGGAGCCC
CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACACATGCAG
GAGGCGGTTGGCAGCGCTGCAGCCGGAGTCCCCCTTACACTGGAGGAACGGAGACCTGTGAC
CAGACAGAGGCTGACAGATGGACAGAATCTCCCGTAGAAGGTTTGGTTTTGAAATGCCCCGGG
GGCAGCAAACTGACATGGTTGAATGATAGCATTTCACTCTGCGTTCTCTAGATCTGAGCAA
GCTGTGAGTTCTACCCCCACCGGTGATATACATGAGCTAACTTTTAAATGTGACAAAA
GGCATCTCCAGATTCCAGACCTGCCGCATGACTTTTCTGAAGGCTTGCTTTTCCCTCGC
CTTTCTCTGAAGGTCGCATTAGGCGAGTCACATGGAGCATCTCAATTTGCAATTTAGTTT
TACAGTGAATGAAGCTTTAAGTCTCATCCAGCATTCTAATGCCAGGTTGCTGTGAGGTAAC
TTTTGAAGTAGATATATTACCTGGTCTGCTATCCTTAGTCATAACTCTGCGGTACAGGTA
TTGAGAAATGATCATCGGTACTTCCCTCCACACCATAACGATAAAGCAAGACATTTTATAACG
ATACCAGAGTCACATATGTGGTCTCCTGAAATAACGCATTGAAATCATGCAGTGCAGTA
TATTTTCTAAGTTTGTGAAACGAGGTTTTTCTTTAAAAAAATATAGACAGGTTCACT
AAATTTGATTAGTCAGAAATCTTAGACTGAAAGAACCTAAACAAAAAAATATTTTAAAGATA
TAAATATATGCTGTATATGTATGTAATTTATTTAGGCTATAATACATTTCTTATTTTCG
ATTTTCAATAAAATGCTCTAATACAAAAA